FIG. 1

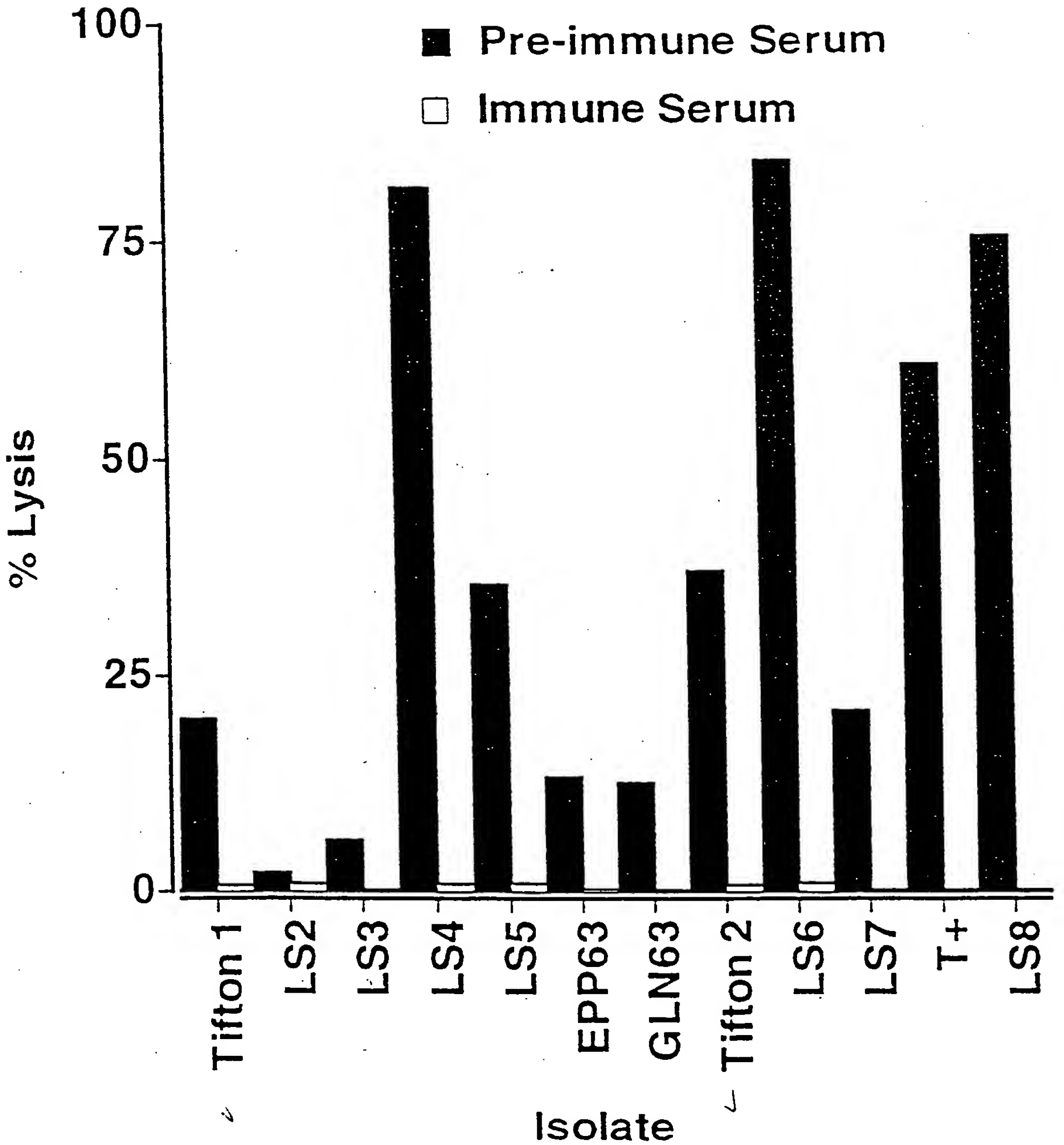

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FIG. 2

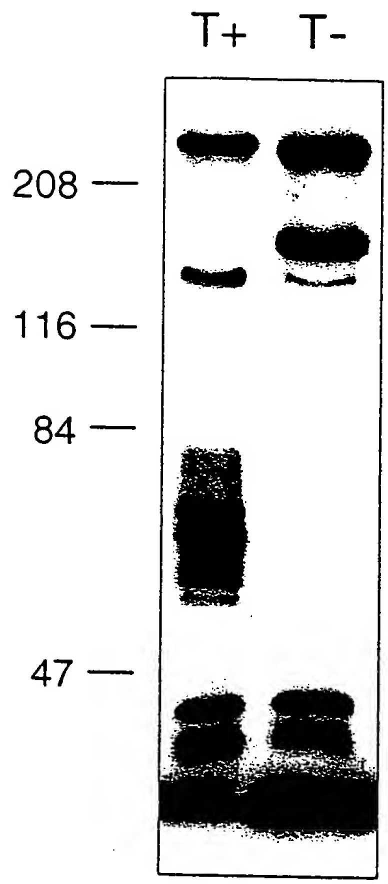


FIG 3-1

Appendix A update-July 1999

Bases 1-1200
Amino acids 1-400

```
   1 ATGTCCAATATAAATGTAATTAAATCTAATATTCAAGCAGGCTTGAATTCAACAAAGTCT    60
   1  M  S  N  I  N  V  I  K  S  N  I  Q  A  G  L  N  S  T  K  S    20

  61 GGATTAAAAAATCTTTACTTGGCTATTCCCAAAGATTATGATCCGCAAAAAGGTGGGACT   120
  21  G  L  K  N  L  Y  L  A  I  P  K  D  Y  D  P  Q  K  G  G  T    40

 121 TTAAATGATTTTATTAAAGCTGCTGATGAATTAGGTATTGCTCGTTTAGCAGAAGAGCCT   180
  41  L  N  D  F  I  K  A  A  D  E  L  G  I  A  R  L  A  E  E  P    60

 181 AATCACACTGAAACAGCAAAAAAATCTGTTGACACAGTAAATCAGTTTCTCTCTCTCACA   240
  61  N  H  T  E  T  A  K  K  S  V  D  T  V  N  Q  F  L  S  L  T    80

 241 CAAACTGGTATTGCTATTTCTGCAACAAAATTAGAAAAGTTCTTACAAAAACATTCTACC   300
  81  Q  T  G  I  A  I  S  A  T  K  L  E  K  F  L  Q  K  H  S  T   100

 301 AATAAGTTAGCCAAAGGGTTAGACAGTGTAGAAAATATTGATCGTAAATTAGGTAAAGCA   360
 101  N  K  L  A  K  G  L  D  S  V  E  N  I  D  R  K  L  G  K  A   120

 361 AGTAATGTATTATCAACATTAAGCTCTTTTTTGGGCACTGCATTAGCGGGTATAGAACTT   420
 121  S  N  V  L  S  T  L  S  S  F  L  G  T  A  L  A  G  I  E  L   140

 421 GATTCTTTAATCAAAAAAGGTGATGCTGCACCTGATGCTTTGGCTAAAGCTAGTATTGAC   480
 141  D  S  L  I  K  K  G  D  A  A  P  D  A  L  A  K  A  S  I  D   160

 481 TTGATTAATGAGATAATTGGTAATCTATCTCAGAGTACTCAAACGATTGAAGCATTTTCT   540
 161  L  I  N  E  I  I  G  N  L  S  Q  S  T  Q  T  I  E  A  F  S   180

 541 TCACAGTTAGCAAAGTTAGGTTCTACTATATCGCAGGCTAAAGGCTTCTCTAATATAGGA   600
 181  S  Q  L  A  K  L  G  S  T  I  S  Q  A  K  G  F  S  N  I  G   200

 601 AACAAGTTGCAAAACTTAAATTTTTCTAAAACAAATCTTGGTTTGGAAATAATTACTGGT   660
 201  N  K  L  Q  N  L  N  F  S  K  T  N  L  G  L  E  I  I  T  G   220

 661 TTGCTATCAGGCATTTCTGCAGGCTTTGCTTTAGCGGATAAAAATGCATCGACTGGCAAA   720
 221  L  L  S  G  I  S  A  G  F  A  L  A  D  K  N  A  S  T  G  K   240

 721 AAAGTTGCTGCAGGTTTTGAATTAAGCAATCAAGTTATTGGTAATGTAACAAAAGCAATT   780
 241  K  V  A  A  G  F  E  L  S  N  Q  V  I  G  N  V  T  K  A  I   260

 781 TCTTCATATGTTTTAGCACAACGTGTTGCTGCTGGTCTATCAACTACTGGTGCTGTTGCT   840
 261  S  S  Y  V  L  A  Q  R  V  A  A  G  L  S  T  T  G  A  V  A   280

 841 GCTTTAATTACTTCATCGATTATGTTGGCAATTAGTCCTTTGGCATTTATGAATGCAGCA   900
 281  A  L  I  T  S  S  I  M  L  A  I  S  P  L  A  F  M  N  A  A   300

 901 GATAAATTCAATCATGCTAATGCTCTTGATGAGTTTGCAAAACAATTCCGAAAATTTGGC   960
 301  D  K  F  N  H  A  N  A  L  D  E  F  A  K  Q  F  R  K  F  G   320

 961 TATGATGGGGATCATTTATTGGCTGAATATCAGCGTGGTGTGGGTACTATTGAAGCTTCA  1020
 321  Y  D  G  D  H  L  L  A  E  Y  Q  R  G  V  G  T  I  E  A  S   340

1021 TTAACTACAATTAGTACGGCATTAGGTGCAGTTTCTGCTGGTGTTTCCGCTGCTGCTGTA  1080
 341  L  T  T  I  S  T  A  L  G  A  V  S  A  G  V  S  A  A  A  V   360

1081 GGATCTGCTGTTGGTGCACCGATTGCACTATTAGTTGCAGGTGTTACAGGATTGATCTCT  1140
 361  G  S  A  V  G  A  P  I  A  L  L  V  A  G  V  T  G  L  I  S   380

1141 GGAATTTTAGAAGCGTCTAAACAGGCAATGTTTGAAAGTGTTGCTAACCGTTTACAAGGT  1200
 381  G  I  L  E  A  S  K  Q  A  M  F  E  S  V  A  N  R  L  Q  G   400
```

moxA + MoxA

FIG 3-2

Appendix A update-July 1999, continued

Bases 1201-2400
Amino acids 401-800

```
1201 AAAATTTTAGAGTGGGAAAAGCAAAATGGCGGTCAGAACTATTTTGATAAAGGCTATGAT  1260
 401  K  I  L  E  W  E  K  Q  N  G  G  Q  N  Y  F  D  K  G  Y  D   420

1261 TCTCGTTATGCTGCTTATTTAGCTAATAACTTAAAATTTTTGTCTGAGCTAAATAAAGAG  1320
 421  S  R  Y  A  A  Y  L  A  N  N  L  K  F  L  S  E  L  N  K  E   440

1321 TTGGAAGCTGAACGTGTTATTGCAATCACCCAACAACGTTGGGATAATAATATTGGTGAG  1380
 441  L  E  A  E  R  V  I  A  I  T  Q  Q  R  W  D  N  N  I  G  E   460

1381 TTAGCAGGTATTACCAAATTGGGTGAACGCATTAAGAGCGGAAAAGCTTATGCAGATGCT  1440
 461  L  A  G  I  T  K  L  G  E  R  I  K  S  G  K  A  Y  A  D  A   480

1441 TTTGAAGATGGCAAGAAAGTTGAAGCTGGTTCCAATATTACTTTGGATGCTAAAACTGGT  1500
 481  F  E  D  G  K  K  V  E  A  G  S  N  I  T  L  D  A  K  T  G   500

1501 ATCATAGACATTAGTAATTCAAATGGGAAAAAAACGCAAGCGTTGCATTTCACTTCGCCT  1560
 501  I  I  D  I  S  N  S  N  G  K  K  T  Q  A  L  H  F  T  S  P   520

1561 TTGTTAACAGCAGGAACTGAATCACGTGAACGTTTAACTAATGGTAAATACTCTTATATT  1620
 521  L  L  T  A  G  T  E  S  R  E  R  L  T  N  G  K  Y  S  Y  I   540

1621 AATAAGTTAAAATTCGGACGTGTAAAAAACTGGCAAGTTACAGATGGAGAGGCTAGTTCT  1680
 541  N  K  L  K  F  G  R  V  K  N  W  Q  V  T  D  G  E  A  S  S   560

1681 AAATTAGATTTCTCTAAAGTTATTCAGCGTGTAGCCGAGACAGAAGGCACAGACGAGATT  1740
 561  K  L  D  F  S  K  V  I  Q  R  V  A  E  T  E  G  T  D  E  I   580

1741 GGTCTAATAGTAAATGCAAAAGCTGGCAATGACGATATCTTTGTTGGTCAAGGTAAAATG  1800
 581  G  L  I  V  N  A  K  A  G  N  D  D  I  F  V  G  Q  G  K  M   600

1801 AATATTGATGGTGGAGATGGACACGATCGTGTCTTCTATAGTAAAGACGGAGGATTTGGT  1860
 601  N  I  D  G  G  D  G  H  D  R  V  F  Y  S  K  D  G  G  F  G   620

1861 AATATTACTGTAGATGGTACGAGTGCAACAGAAGCAGGCAGTTATACAGTTAATCGTAAG  1920
 621  N  I  T  V  D  G  T  S  A  T  E  A  G  S  Y  T  V  N  R  K   640

1921 GTTGCTCGAGGTGATATCTACCATGAAGTTGTGAAGCGTCAAGAAACCAAGGTGGGTAAA  1980
 641  V  A  R  G  D  I  Y  H  E  V  V  K  R  Q  E  T  K  V  G  K   660

1981 CGTACTGAAACTATCCAGTATCGTGATTATGAATTAAGAAAAGTTGGGTATGGTTATCAG  2040
 661  R  T  E  T  I  Q  Y  R  D  Y  E  L  R  K  V  G  Y  G  Y  Q   680

2041 TCTACCGATAATTTGAAATCAGTAGAAGAAGTAATTGGTTCTCAATTTAATGATGTATTC  2100
 681  S  T  D  N  L  K  S  V  E  E  V  I  G  S  Q  F  N  D  V  F   700

2101 AAAGGTTCTAAATTCAACGACATATTCCATAGTGGTGAAGGTGATGATTTACTCGATGGT  2160
 701  K  G  S  K  F  N  D  I  F  H  S  G  E  G  D  D  L  L  D  G   720

2161 GGTGCTGGTGACGACCGCTTGTTTGGTGGTAAAGGCAACGATCGACTTTCTGGAGATGAA  2220
 721  G  A  G  D  D  R  L  F  G  G  K  G  N  D  R  L  S  G  D  E   740

2221 GGCGATGATTTACTCGATGGCGGTTCTGGTGATGATGTATTAAATGGTGGTGCTGGTAAT  2280
 741  G  D  D  L  L  D  G  G  S  G  D  D  V  L  N  G  G  A  G  N   760

2281 GATGTCTATATCTTTCGGAAAGGTGATGGTAATGATACTTTGTACGATGGCACGGGCAAT  2340
 761  D  V  Y  I  F  R  K  G  D  G  N  D  T  L  Y  D  G  T  G  N   780

2341 GATAAATTAGCATTTGCAGATGCAAATATATCTGATATTATGATTGAACGTACCAAAGAG  2400
 781  D  K  L  A  F  A  D  A  N  I  S  D  I  M  I  E  R  T  K  E   800
```

FIG 3-3

Appendix A update-July 1999, continued

Bases 2401-2784
Amino acids 801-927

```
2401 GGTATTATAGTTAAACGAAATGATCATTCAGGTAGTATTAACATACCAAGATGGTACATA  2460
 801  G  I  I  V  K  R  N  D  H  S  G  S  I  N  I  P  R  W  Y  I    820

2461 ACATCAAATTTACAAAATTATCAAAGTAATAAAACAGATCATAAAATTGAGCAACTAATT  2520
 821  T  S  N  L  Q  N  Y  Q  S  N  K  T  D  H  K  I  E  Q  L  I    840

2521 GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTTTGCAAGATAAGAAA  2580
 841  G  K  D  G  S  Y  I  T  S  D  Q  I  D  K  I  L  Q  D  K  K    860

2581 GATGGTACAGTAATTACATCTCAAGAATTGAAAAAGCTTGCTGATGAGAATAAGAGCCAA  2640
 861  D  G  T  V  I  T  S  Q  E  L  K  K  L  A  D  E  N  K  S  Q    880

2641 AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGGTCAATGGCACTA  2700
 881  K  L  S  A  S  D  I  A  S  S  L  N  K  L  V  G  S  M  A  L    900

2701 TTTGGTACAGCAAATAGTGTGAGTTCTAACGCCTTACAGCCAATTACACAACCAACTCAA  2760
 901  F  G  T  A  N  S  V  S  S  N  A  L  Q  P  I  T  Q  P  T  Q    920

2761 GGAATTTTGGCTCCAAGTGTTTAG           SEQ ID NO: 1                2784
 921  G  I  L  A  P  S  V  *            SEQ ID NO: 2                928
```

FIG. 4

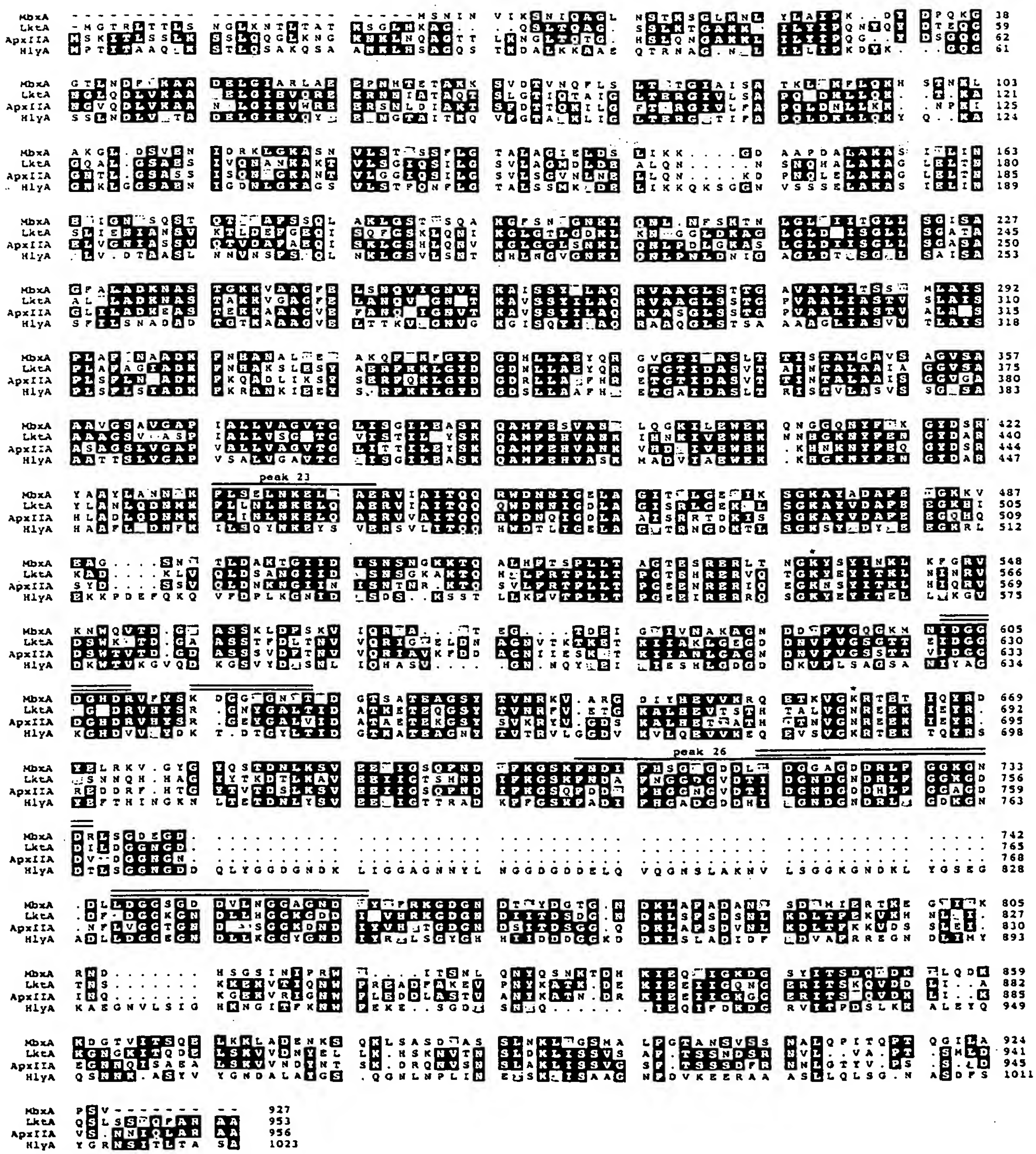


FIG. 5

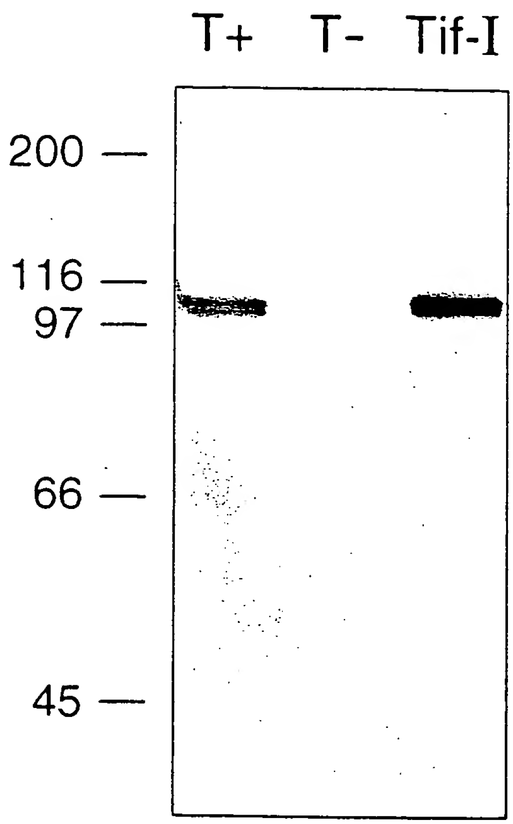

T+
T-
Tif-I
200
116
97
66
45

FIG. 6

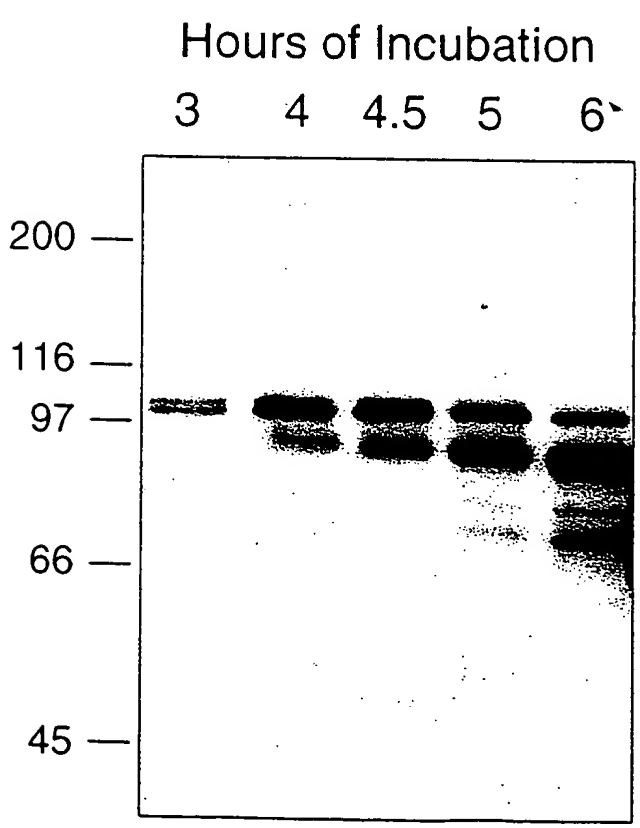
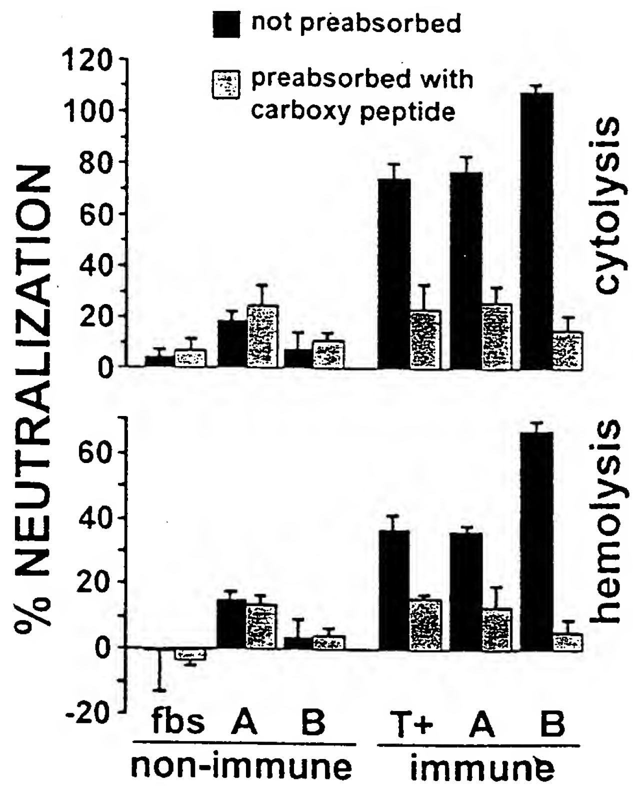

Hours of Incubation
3
4
4.5
5
6
200
116
97
66
45

FIG. 7



not preabsorbed
preabsorbed with carboxy peptide
% NEUTRALIZATION
120
100
80
60
40
20
0
-20
cytolysis
hemolysis
fbs
A
B
T+
A
B
non-immune
immune

mbxB
mbxβ

FIG 8-1

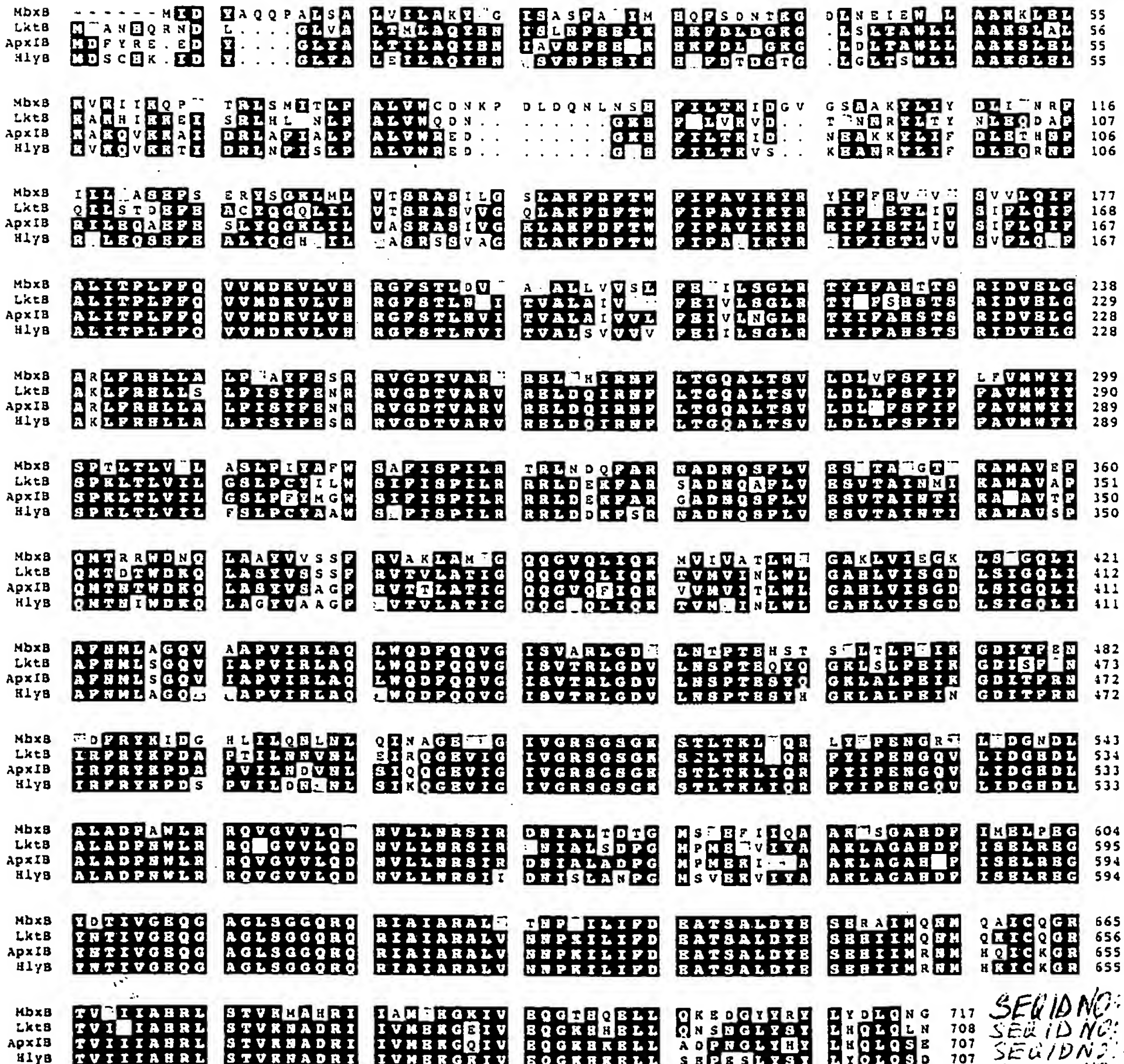
1	ATGGGTGGTGATACTTCTTTAATTAGACTTAATTTACAAACCCTTAATAGTAATTTAGTT	60
1	M G G D T S L I [illegible] L N L Q T L N S N L V	20
61	ATGATAGATTATGCTCAACAACCTGCTCTATCTGCTCTGGTTATCCTTGCCAAATACTAT	120
21	M I D Y A Q Q P A L S A L V I L A K Y Y	40
121	GGTATTTCTGCAAGTCCAGCAGACATTATGCATCAGTTTTCTGATAATACAAAAGGAGAC	180
41	G I S A S P A D I M H Q F S D N T K G D	60
181	CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAAGGTAAAGATTATA	240
61	L N E I E W M L A A K K L E L K V K I I	80
241	AAACAGCCTTTAACTCGATTGTCAATGATAACACTTCCTGCTTTGGTGTGGTGTGATAAT	300
81	K Q P L T R L S M I T L P A L V W C D N	100
301	AAGCCCGATTTAGATCAAAATTTAAACTCTCATTTTATACTAACTAAAATTGATGGGGTG	360
101	K P D L D Q N L N S H F I L T K I D G V	120
361	GGATCTGCTGCAAAATATCTCATCTACGATTTGATTGAGAATCGTCCCATAATATTAGAT	420
121	G S A A K Y L I Y D L I E N R P I I L D	140
421	GCAAGTGAGTTTTCTGAAAGATATTCTGGTAAGTTAATGCTAGTAACTTCCCGTGCGTCA	480
141	A S E F S E R Y S G K L M L V T S R A S	160
481	ATATTGGGTTCATTGGCTAAATTTGATTTTACTTGGTTTATTCCTGCGGTAATCAAATAT	540
161	I L G S L A K F D F T W F I P A V I K Y	180
541	CGTTATATTTTTTTTGAAGTCATCGTTATTTCAGTGGTGCTACAGATTTTTGCTCTGATT	600
181	R Y I F F E V I V I S V V L Q I F A L I	200
601	ACGCCATTGTTTTTTCAGGTTGTGATGGATAAGGTATTGGTGCATCGTGGTTTTTCTACT	660
201	T P L F F Q V V M D K V L V H R G F S T	220
661	CTGGATGTGGTAGCGATTGCCTTGTTGGTAGTAAGTTTATTTGAAGTCATTTTAAGTGGT	720
221	L D V V A I A L L V V S L F E V I L S G	240
721	CTACGCACTTATATTTTTGCTCATACAACCTCTCGAATTGATGTAGAGCTAGGAGCACGA	780
241	L R T Y I F A H T T S R I D V E L G A R	260
781	TTATTTCGTCATCTATTAGCTCTACCGCTTGCTTATTTTGAGAGTAGAAGAGTAGGCGAT	840
261	L F R H L L A L P L A Y F E S R R V G D	280
841	ACAGTTGCACGTATACGTGAATTGGAACATATCCGCAATTTCTTAACTGGTCAAGCTCTC	900
281	T V A R I R E L E H I R N F L T G Q A L	300
901	ACTTCAGTTTTAGATTTGGTGTTTTCTTTTATATTCTTGTTTGTAATGTGGTATTACAGC	960
301	T S V L D L V F S F I F L F V M W Y Y S	320
961	CCTACTTTAACACTGGTAGTTTTGGCATCATTACCAATATATGCGTTTTGGTCTGCCTTT	1020
321	P T L T L V V L A S L P I Y A F W S A F	340
1021	ATTAGCCCAATTTTACGCACTCGACTAAATGATCAATTTGCACGCAATGCAGATAATCAA	1080
341	I S P I L R T R L N D Q F A R N A D N Q	360
1081	TCTTTTTTAGTGGAAAGTATTACTGCGGTTGGTACGGTAAAAGCAATGGCAGTTGAACCT	1140
361	S F L V E S I T A V G T V K A M A V E P	380
1141	CAAATGACCCGTCGCTGGGATAATCAATTAGCAGCTTATGTGGTTTCTAGTTTTCGGGTA	1200
381	Q M T R R W D N Q L A A Y V V S S F R V	400
1201	GCTAAGTTGGCAATGGTTGGGCAGCAAGGAGTACAACTCATTCAAAAGATGGTTATTGTG	1260
401	A K L A M V G Q Q G V Q L I Q K M V I V	420
1261	GCAACTCTATGGATTGGTGCAAAATTGGTAATTGAAGGCAAGCTATCGGTAGGTCAATTA	1320
421	A T L W I G A K L V I E G K L S V G Q L	440

FIG 8-2

```
1321 ATAGCATTTAATATGCTGGCAGGTCAGGTGGCCGCTCCTGTTATCCGCCTGGCACAGCTA  1380
 441  I  A  F  N  M  L  A  G  [illegible]  V  A  A  P  V  I  R  L  A  Q  L   460

1381 TGGCAAGATTTTCAGCAAGTAGGTATTTCAGTGGCGAGATTGGGTGATATTTTAAATACT  1440
 461  W  Q  D  F  Q  Q  V  G  I  S  V  A  R  L  G  D  I  L  N  T   480

1441 CCAACTGAGCATTCTACATCTCGCTTAACTTTACCTGATATTAAGGGTGATATTACATTT  1500
 481  P  T  E  H  S  T  S  R  L  T  L  P  D  I  K  G  D  I  T  F   500

1501 GAAAATGTTGATTTTCGCTACAAAATAGATGGGCATTTAATATTACAGAATTTAAATTTA  1560
 501  E  N  V  D  F  R  Y  K  I  D  G  H  L  I  L  Q  N  L  N  L   520

1561 CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAGGTAAATCAACA  1620
 521  Q  I  N  A  G  E  I  L  G  I  V  G  R  S  G  S  G  K  S  T   540

1621 TTGACAAAATTAGTACAGCGTTTATATGTACCAGAAAATGGGCGAATATTAGTTGATGGA  1680
 541  L  T  K  L  V  Q  R  L  Y  V  P  E  N  G  R  I  L  V  D  G   560

1681 AACGATTTGGCATTAGCTGATCCCGCTTGGCTGCGTCGCCAAGTGGGTGTTGTTTTGCAG  1740
 561  N  D  L  A  L  A  D  P  A  W  L  R  R  Q  V  G  V  V  L  Q   580

1741 GAAAATGTGTTACTCAATCGTAGTATTCGAGATAATATTGCCCTAACTGATACGGGCATG  1800
 581  E  N  V  L  L  N  R  S  I  R  D  N  I  A  L  T  D  T  G  M   600

1801 TCATTAGAGTTTATTATCCAGGCTGCCAAGATGTCTGGGGCACATGACTTTATTATGGAA  1860
 601  S  L  E  F  I  I  Q  A  A  K  M  S  G  A  H  D  F  I  M  E   620

1861 TTGCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTCAGGTGGACAA  1920
 621  L  P  E  G  Y  D  T  I  V  G  E  Q  G  A  G  L  S  G  G  Q   640

1921 CGCCAGCGTATCGCTATTGCGCGTGCTTTAATTACCAATCCGCGTATTTTGATTTTTGAT  1980
 641  R  Q  R  I  A  I  A  R  A  L  I  T  N  P  R  I  L  I  F  D   660

1981 GAAGCTACTAGTGCATTAGACTATGAGTCGGAAAGGGCTATTATGCAAAATATGCAGGCA  2040
 661  E  A  T  S  A  L  D  Y  E  S  E  R  A  I  M  Q  N  M  Q  A   680

2041 ATTTGCCAAGGTAGAACAGTGTTGATTATTGCACATCGCTTATCTACCGTAAAAATGGCA  2100
 681  I  C  Q  G  R  T  V  L  I  I  A  H  R  L  S  T  V  K  M  A   700

2101 CATCGCATTATTGCAATGGACAAGGGGAAAATTGTAGAGCAAGGCACACATCAAGAATTG  2160
 701  H  R  I  I  A  M  D  K  G  K  I  V  E  Q  G  T  H  Q  E  L   720

2161 TTGCAAAAAGAAGATGGTTACTATCGTTATTTATATGATTTGCAGAATGGATAAA      2215
 721  L  Q  K  E  D  G  Y  Y  R  Y  L  Y  D  L  Q  N  G  *        739
```

SEQ ID NO: 30
SEQ ID NO: 18

FIG. 9



SEQ ID NO: 18
SEQ ID NO: 19
SEQ ID NO: 20
SEQ ID NO: 21

FIG. 10

```
DNASIS  Translation Editor [11-00 C gene.dna]
      1 ATGACGAAAAAGTTTGCAGAGCTAGGTTTAATTGCATGGCTTTGGTCTAACTCTGATATG     60
      1  M  T  K  K  F  A  E  L  G  L  I  A  W  L  W  S  N  S  D  M      20

     61 CATAAACATTGGACGTTGTCTTTGTTTGCGACCAATGTTATTCCGGCAATTGAGACAGGT    120
     21  H  K  H  W  T  L  S  L  F  A  T  N  V  I  P  A  I  E  T  G      40

    121 CAATATGTTATATTGAAAAGAGAAGATATGCCTGTAGCATATTGTAGTTGGGCTAAACTT    180
     41  Q  Y  V  I  L  K  R  E  D  M  P  V  A  Y  C  S  W  A  K  L      60

    181 AGTTTAGAAAACGAGGTTAAATATATTAACGATGTTACTTCTCTTAAGTTAGATGACTGG    240
     61  S  L  E  N  E  V  K  Y  I  N  D  V  T  S  L  K  L  D  D  W      80

    241 CAGTCAGGTGACCGAAACTGGTTTATTGACTGGATTGCTCCATTTGGCGATAGTCTTACA    300
     81  Q  S  G  D  R  N  W  F  I  D  W  I  A  P  F  G  D  S  L  T     100

    301 CTCACAAAACACATGAGAACGTTATTTTCAGATGAATTGTTTAGAGCGATTCGTGTAGAT    360
    101  L  T  K  H  M  R  T  L  F  S  D  E  L  F  R  A  I  R  V  D     120

    361 GGAAATTCATCGCATGGTAAGATATCTGAATTTTATGGAAAGTCTGTTGATTCAAAATTA    420
    121  G  N  S  S  H  G  K  I  S  E  F  Y  G  K  S  V  D  S  K  L     140

    421 GCCTCAAGAATATTTGCACAATATCACGAAGATTTGACGAGCAAATTGTCAACTCAGAAT    480
    141  A  S  R  I  F  A  Q  Y  H  E  D  L  T  S  K  L  S  T  Q  N     160

    481 AATTTTATTATATCTAAAGATAATTAA                                     507
    161  N  F  I  I  S  K  D  N  *                                       169
```

SEQ ID NO: 31
SEQ ID NO: 32

mbxC
MbxC

FIG. 11

```
MbxC   ---MTKKFAE LGLIAWLWSN SD[illegible]HKHWTLS LFATNVIPAI ETGQY  42
LktC   --MNQSYFNL LGNITWLWMN SSLHKEWSCE LLARNVIPAI ENEQY  43
ApxIC  MSKKINGFEV LGEVAWLWAS SPLHRKWPLS LLAINVLPAI ESNQY  45
HlyC   -MNRNNPLEV LGHVSWLWAS SPLHRNWPVS LFAINVLPAI RANQY  44

MbxC   V[illegible]LKR[illegible]DMPV AYCSWAKLSL ENEVKYINDV TSLKLDDWQS GDRNW  87
LktC   MLLIDNGIPI AYCSWADLNL ETEVKYIKD[illegible] NSLTPE[illegible]WQS GDRRW  88
ApxIC  VLLKRDGFPI A[illegible]CSWANLNL ENEIKYLDDV ASLVADDWTS GDRRW  90
HlyC   ALLTRDNYPV AYCSWANLSL ENEIKYLNDV TSLVAEDWTS GDR[illegible]W  89

MbxC   FIDWIAPFGD SLTLTKHMRT LFSDELFRAI RVDGNSS.HG KISEF  131
LktC   IIDW[illegible]APFGH SQLLYKKMCQ K[illegible]PDM[illegible]VRSI RFYPKQKELG KIAYF  133
ApxIC  FIDWIAPFGD SAALYKHMRD NFPNELFRAI RVDPDSR.VG KISEF  134
HlyC   FIVWIAPFGD NGALYK[illegible]MRK KFPDELFRAI RVDPKTH.VG K[illegible]SEF  133

MbxC   [illegible]GKS[illegible]DSKLA S[illegible]IFAQYHE[illegible] LTSKLSTQNN FIISKDN-  168
LktC   KGGK[illegible]DKKTA KKRPDTYQEE LATALKNEFN FIKK----  167
ApxIC  HGGKIDKKLA SKIFQQYHFE LMSELKNKQN FKFSLVNS  172
HlyC   HGGKIDKQLA NKIPKQYHHE LITEVKNKSD FNFSLTG-  170
```

SEQ ID NO: 32
SEQ ID NO: 33
SEQ ID NO: 34
SEQ ID NO: 35

```
   1 ATGTTTATACAAGCACTTAAAGATTTTTTTATTCGCTATATAACCGTTTGGCGCAATACA     60
   1  M  F  I  Q  A  L  K  D  [illegible]  F  I  R  Y  I  T  V  W  R  N  T     20

  61 TGGGCAGTTCGAGACCAACTAACCCCTCCTAAGCGTACTAAAGAAGAACTCGCTTTTCTT    120
  21  W  A  V  R  D  Q  L  T  P  P  K  R  T  K  E  E  L  A  F  L     40

 121 CCTGCACATCTAGAACTCACTGACACACCTGTATCCAGATCTTCTAAGTGGACAGCTAGA    180
  41  P  A  H  L  E  L  T  D  T  P  V  S  R  S  S  K  W  T  A  R     60

 181 ATAATCATGATATTTGTCCTATTTGCTTTGCTATGGTCTTGGGTTGGACAGATTGACATT    240
  61  I  I  M  I  F  V  L  F  A  L  L  W  S  W  V  G  Q  I  D  I     80

 241 GTTGCTACAGCTTCAGGTAAAATTTCTTCAGGTAGCCGTAGCAAGACTATTCAATCTTTG    300
  81  V  A  T  A  S  G  K  I  S  S  G  S  R  S  K  T  I  Q  S  L    100

 301 GAAACAGCGATAGTTAAAGCAGTTTATGTACGTGATGGTCAAAATGTTCAACAAGGTGAA    360
 101  E  T  A  I  V  K  A  V  Y  V  R  D  G  Q  N  V  Q  Q  G  E    120

 361 ATATTAGTAGATTTAGTGGGAATCGGTTCAGATAGTGATGTTGCTCAGTCCGAGAAAGCC    420
 121  I  L  V  D  L  V  G  I  G  S  D  S  D  V  A  Q  S  E  K  A    140

 421 CTTCGAGCAGCGCAATTATCTAAGCTACGCCTTGAAGCAATTTTATCAGCATTAAATCAC    480
 141  L  R  A  A  Q  L  S  K  L  R  L  E  A  I  L  S  A  L  N  H    160

 481 CGTATTAATCCTCAGATTGATGTAGCATATGCAAAGTCTTTAAATATTTCAGAATCGGAA    540
 161  R  I  N  P  Q  I  D  V  A  Y  A  K  S  L  N  I  S  E  S  E    180

 541 ATTAATGAAGCTCAAACTTTAGCCCAAAATCAATATCAAGCATGGTTAGCACAAGATGAA    600
 181  I  N  E  A  Q  T  L  A  Q  N  Q  Y  Q  A  W  L  A  Q  D  E    200

 601 CAACTAAAATTAACCTTAAAAGGACATCAAGCAGAATTACAATCTGCTCGATCCCAAGAA    660
 201  Q  L  K  L  T  L  K  G  H  Q  A  E  L  Q  S  A  R  S  Q  E    220

 661 CAAAAGTTGGTTTCAGTTGGTGCAATTGAACATCAAAAGACTGATGATTATCGGAGTCTC    720
 221  Q  K  L  V  S  V  G  A  I  E  H  Q  K  T  D  D  Y  R  S  L    240

 721 AAAGCAGAAAATTTTATATCTGAGCATGCTTATCTAGAACAAGAAAGCAAATTACTTAGC    780
 241  K  A  E  N  F  I  S  E  H  A  Y  L  E  Q  E  S  K  L  L  S    260

 781 AATCAAAATGATTTACAAAGTACACGTAGTCAGATTCAAAAAATACAGGCTGCAATCATG    840
 261  N  Q  N  D  L  Q  S  T  R  S  Q  I  Q  K  I  Q  A  A  I  M    280

 841 CAAGCTGAACAGAACCGTATGTTATATACTCAAAATCTAAAACGTGATACATTAGAATCT    900
 281  Q  A  E  Q  N  R  M  L  Y  T  Q  N  L  K  R  D  T  L  E  S    300

 901 TTACGCCAAACCAATGAACAGATTAATCAATATACTGGTCAAACTAATAAAGCTAAGCAG    960
 301  L  R  Q  T  N  E  Q  I  N  Q  Y  T  G  Q  T  N  K  A  K  Q    320

 961 CGACAGAAATTGCTGAGTATTAAATCACCTGTTAATGGTACTATACAAGAGCTAACAGCT   1020
 321  R  Q  K  L  L  S  I  K  S  P  V  N  G  T  I  Q  E  L  T  A    340

1021 TATACTTTAGGTGGAGTTGTACAAGCAGCACAAAAAATTATGGTTGTGGCACCTAACGAT   1080
 341  Y  T  L  G  G  V  V  Q  A  A  Q  K  I  M  V  V  A  P  N  D    360

1081 AATCAAGTGGAAGTAGAGGTATTAGTGCTAAATAAAGATATCGGCTTTGTAAAAGCTGGG   1140
 361  N  Q  V  E  V  E  V  L  V  L  N  K  D  I  G  F  V  K  A  G    380

1141 CAGAATGTTATCATCAAAATCGAGAGTTTTCCTTATACACGTTATGGTTATTTAACAGGT   1200
 381  Q  N  V  I  I  K  I  E  S  F  P  Y  T  R  Y  G  Y  L  T  G    400

1201 AAAATAAAAAGTATTAGTCATGATGCTATAGAACATCAACATTTAGGTCTAGTGTATACT   1260
 401  K  I  K  S  I  S  H  D  A  I  E  H  Q  H  L  G  L  V  Y  T    420

1261 GCACTTGTTTCTCTTGATAAAAGCACATTAAATATAGATGGAGTAACAATCAACTTAACG   1320
 421  A  L  V  S  L  D  K  S  T  L  N  I  D  G  V  T  I  N  L  T    440
```

(mbx)
(mbx)

FIG 12-1

1321 CCAGGAATGAATGTTACTGCTGAAATTAAAAACAGGTAAACGTCGTGTTTTGGATTATATA 1380
441 P G M N V T A E [illegible] K T G K R R V L D Y I 460

1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTCGAGAACGCTAA 1428
461 L S P L Q T K V D E S F R E R * 476

SEQ ID NO: 36
SEQ ID NO 37

FIG. 12-2

FIG. 13

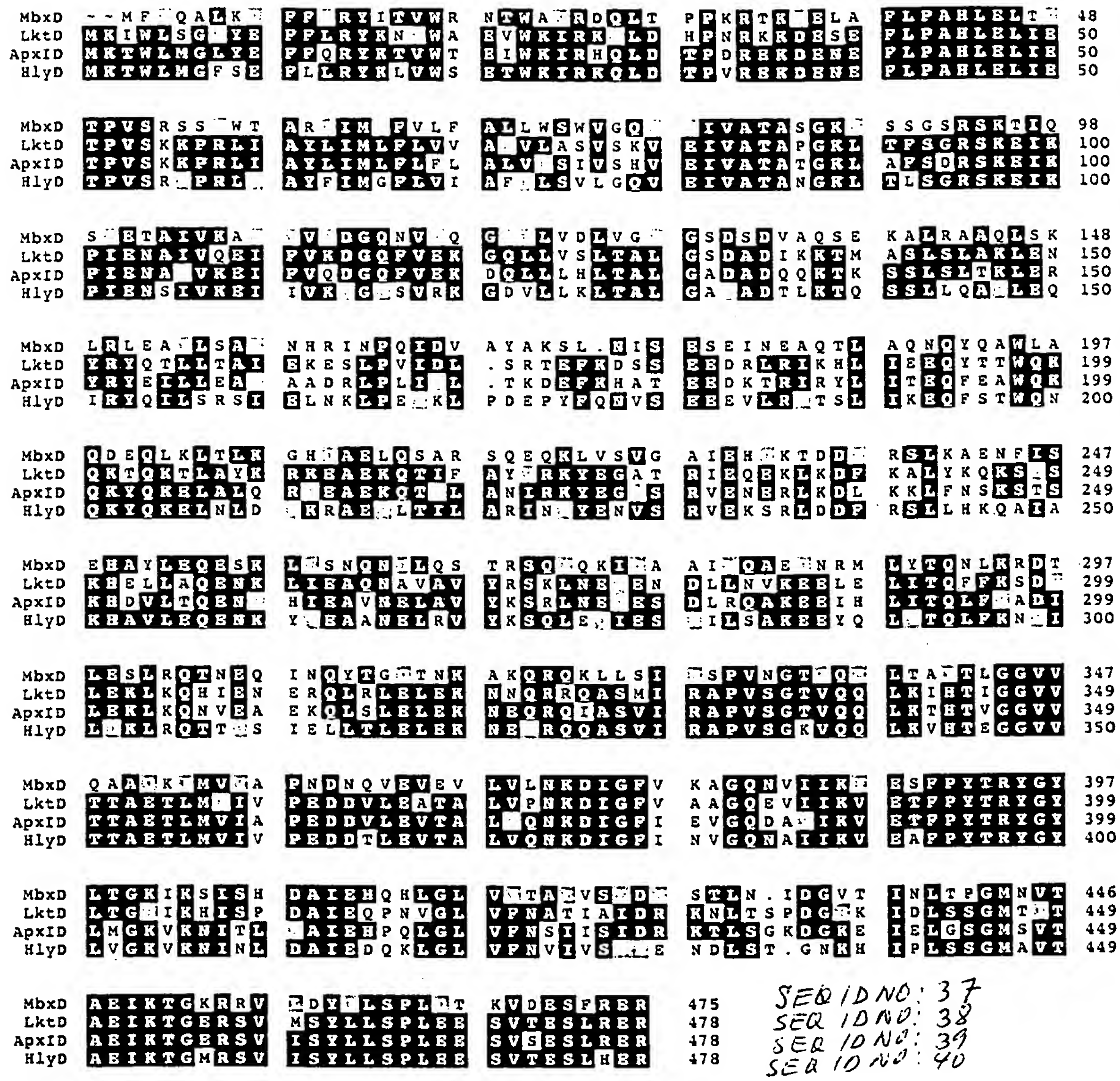
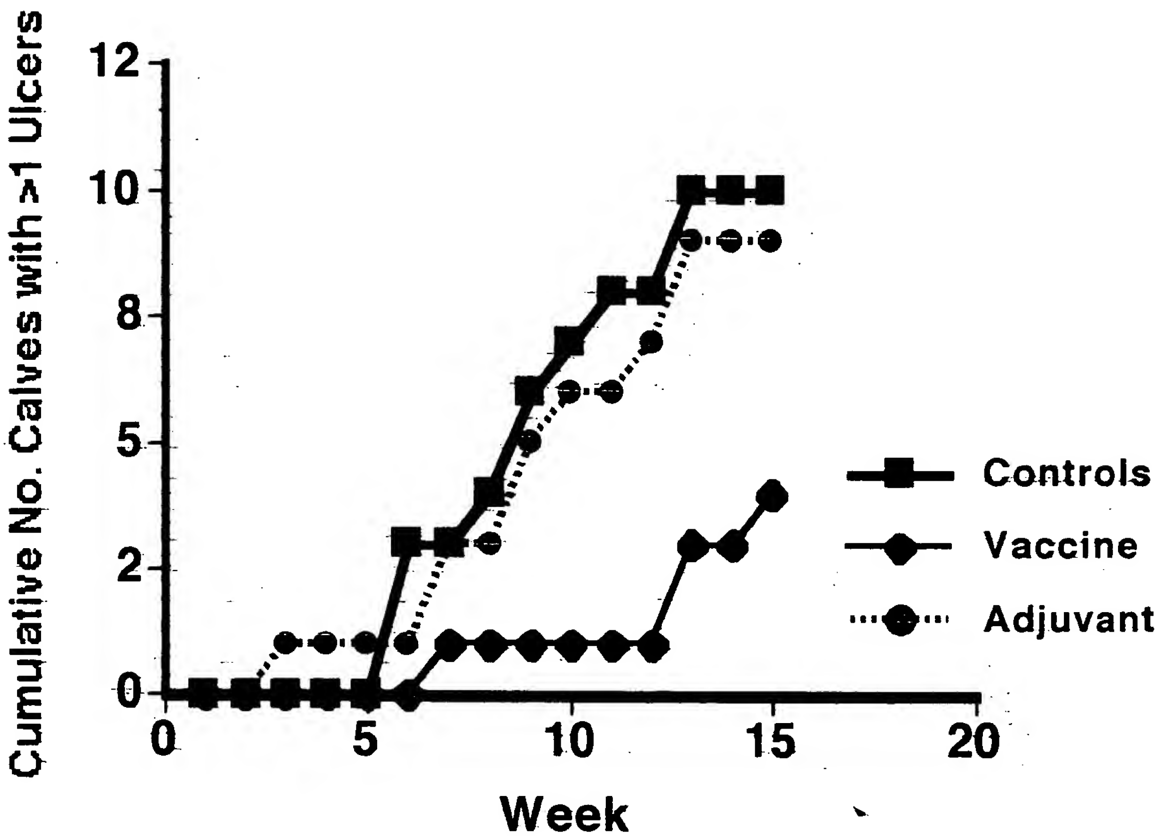

MbxD
LktD
ApxID
HlyD
SEQ ID NO: 37
SEQ ID NO: 38
SEQ ID NO: 39
SEQ ID NO: 40

FIG. 14

Cumulative Number of
Calves With Severe Ulcers



Number of calves with ulcers with clinical scores >+2

F1615

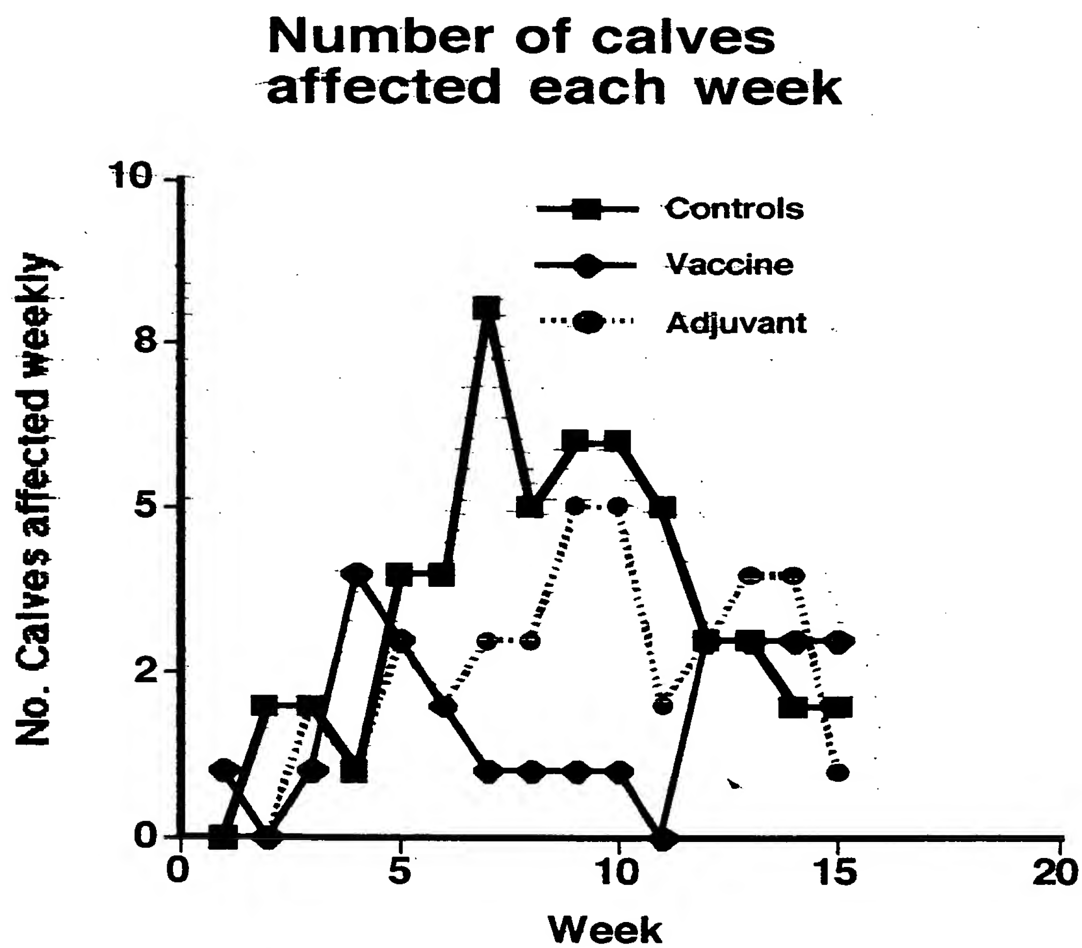
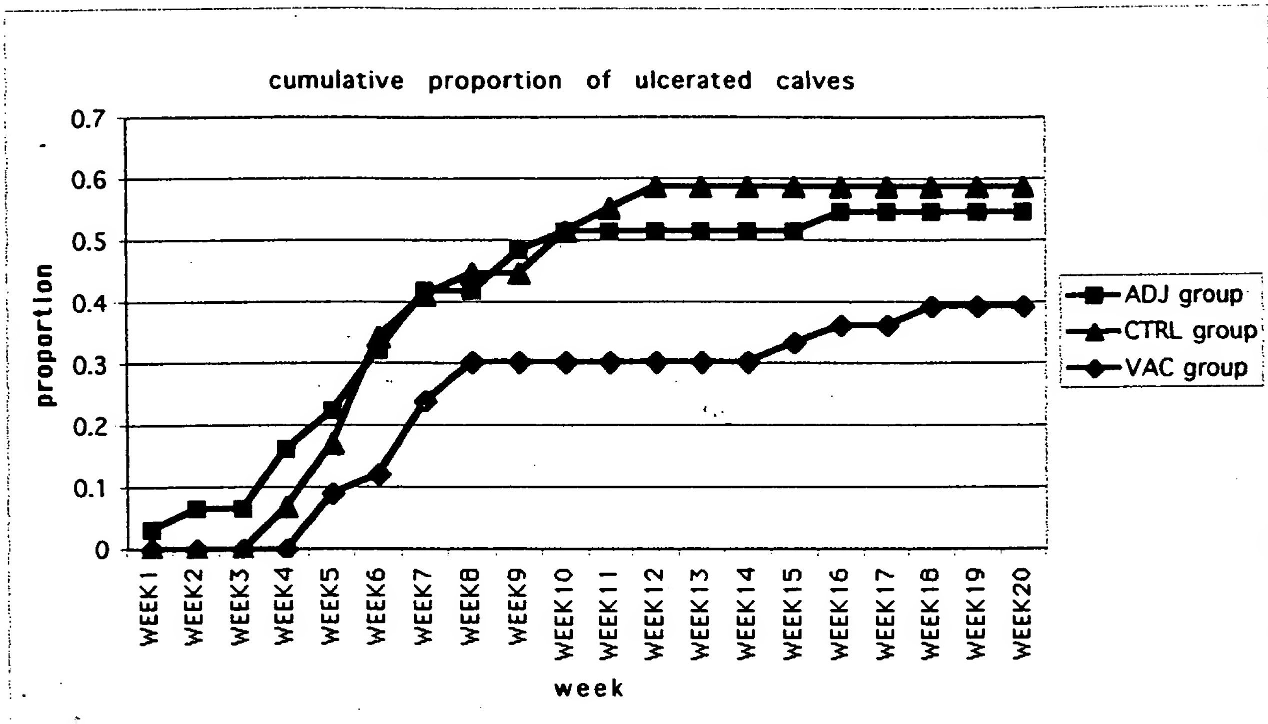


Figure 15
Number of calves affected weekly in 1 group of vaccinated calves and in controls.

FIG. 16



Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').